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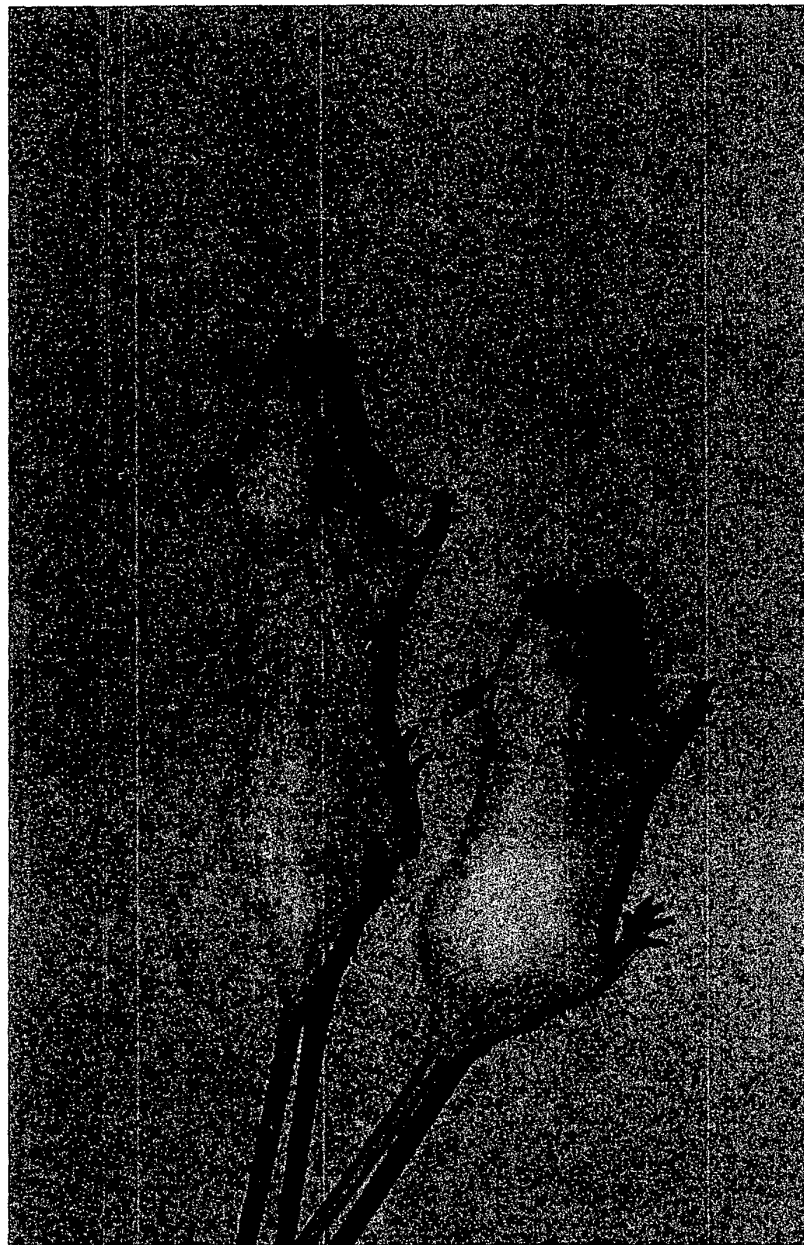


Fig. 1

Fig. 2a

**Fig. 2b**



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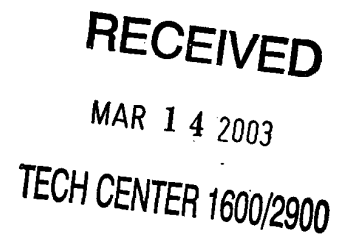
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HS-HMC-Dis3	183	AIQEGIPAPTCEEYVKTLT	----	ANPELIDRLACLSEEGNEIES	----	GKIIIFSEHLPLSKL		
MM-hmc-Dis3	183	AVQEGIPAPTCEEYVKSLT	----	ANPELIDRLAYLSDEMNEIES	----	GKIIIFSEHLPLSKL		
CE-Q17632-Dis3	191	HYQH----	VMYLKEYIQNLDP	----	GKQALDDQMAAYESSGNGNE	----	KQIFDEYLSHDRI	
SP-P37202-Dis3	199	AAEQGIQVSTLKDYYQYLP	----	DSEILLDMVSAIADAIASKEQVES	----	GTKNVYELHWSMSRL		
SC-Q08162-Dis3	207	EVESNIITKSLVQYIELLP	----	NADDIRDSIP-QMDSFDKDLERDT	----	FSDFTFPEYYSTARV		
MM-LOBO	107	GDLVVVKLLPEDQWKAVER	----	E----	SNDKEIEATYEADIPE	----	EGCGHHPL	
HS-LOBO	0	----	----	----	----	----	----	
CE-Q09568-LOBO	92	GDVVAVKIKPKEDWLVNYV	----	E----	YVKNWAEH	----	----	
SP-299259	143	NSAK----	REKNNSHQVEADT	----	NN----	ATEMVSSNAKKS	----	VYPLYYDSATV
SC-P24276-SSD1	280	PQQQLSPFRHRGNSRDYNSFNTLEPPAIF	QOQGHKHRASNSSVHSFSSQGNNGGRKSLFAPYLPQANI					
SC-P39112	206	NRVLLRIPHKLPACIHSLI	----	QPESHKKHLPIGTVKNFNSQTN	----	ILPIVARQLITSRY		
	281	291	301	311	321	331	341	
	----	----	----	----	----	----	----	
HS-HMC-Dis3	237	QOGIKSGTYLQGTFRASRENYLEATV	WIHGDNENKEIILQGLKHLNRAVHEDIVAVELLPKS-QWVAPS					
MM-hmc-Dis3	237	QOGIKSGSYLQGTFRASRENYLEATV	WIHGDKKEEKEIILQGIKHLNRAVHEDIVAVELLPRS-QWVAPS					
CE-Q17632-Dis3	242	MEGASGTIKRGNFVSRENYREATVIID	----	DQLTSWFTTG--NNCNRAVNGDTVAVQLLPED-QWTAPE				
SP-P37202-Dis3	257	LACIKNGEVHKGLINISTYNYLEGSVVVP	----	GYNKPVLSGRENLRNAVQGDIVICIQLPQD-QWKTEA				
SC-Q08162-Dis3	264	MGGLKNGVLYQGNIIQISEYNFLEGSVSLP	----	RFSKPVLIIVGQKNLNRAFNGDQVIVELLPQS-EWKAPS				

Fig. 2c

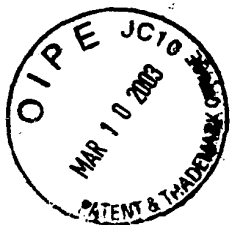
**Fig. 2d**



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**Fig. 2e**



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HS-HMC-Dis3	405	PRNSRYPNHGFVRNLGDVGEKETETEVLSLEHDPVHQPFQAVLSFLP---	KMPWS---	ITEKDM				
MM-hmc-Dis3	405	PRNSRYPNHGFVRNLGDVGEKETETEVLSLEHDPVHQPFQAVLSFLP---	RMPWS---	ITEEDM				
CE-Q17632-Dis3	414	PRDSKYPLGHYVRSIGEMGSRGTENEVLLLEHDIHPAPFSESVDCLP---	REEWEPD---	LTENRG				
SP-P37202-Dis3	428	DASSRYPEGHFVRDLGEMETKEAETEALLEYDVQHRPFPKAVLDCLP---	GHNWKVP---	ADKTH				
SC-Q08162-Dis3	456	PTTHKYPLGHFVRDLGTIESAQAEALLEHDDVEYRFPFSSKVLCECLPAE---	GHDWKAPT---	KLDDPEAVSKD				
MM-LOBO	306	KEDCNFALGQAKSLGQAGEIEPETEGILTTEYGVDFSDFSSEVLECLPQS---	LPWTIP---	PDEV				
HS-LOBO	0							
CE-Q09568-LOBO	237	RAESVYADGRLVKLLGMSGEIDTETERIVVEHQIDHREFSDECLSLPITTAENWKVP---		DAEF				
SP-Z99259	379	SIYSRYPMGVLGEKLGNTDVEAYTNALLLENGISSPFSDEVNLCLP---	PDDWIIIS---	HEEI				
SC-P24276-SSD1	624	PITSLHPFGILVSELGDIHDPDTEIDSILRDNFLSNEYLDQKNPQKEKPSFQPLPLT---		AESL				
SC-P39112	443	LISKIFRKIERKDCDITRDICQDLNEITPNSIPNPLLLNMDLALPASSKLKWOQKLYDLTNIEELQW						
		631	641	651	661	671	681	691
HS-HMC-Dis3	464	KN-----	REDLRHLCICSVDPPGCTDIDDALHCRELEN-----	GN---	LAVGVHIAADVSHFIRLGNALDQE			
MM-hmc-Dis3	464	KN-----	REDLRHLCVCSVDPPGCTDIDDALHCRELSN-----	GN---	LEVGVHIAADVSHFIRPGNALDQE			
CE-Q17632-Dis3	475	PLP-----	RVDLRDLTICSVDPLGCTDIDDALHCKQIGE-----	DL---	FEVGVHIADVTHFVRPGTAIDDE			
SP-P37202-Dis3	490	PLWKN---	RKDFRDKLICSIDPPGQDIDDALHACVLPN-----	GN---	YEVGVHIADVTHFVKPNTSMDSE			
SC-Q08162-Dis3	525	PLLTG---	RKDLRDKLICSIDPPGQDIDDALHAKKLPN-----	GN---	WEVGVHIADVTHFVKPGTALDAE			
MM-LOBO	366	GK-----	RRDLRKDCIFTIDPSTARDLDDALACRRLTD-----	GT---	FEVGVHIADVSYFVPEGSSLDKV			
HS-LOBO	0		KDCIFTIDPSTARDLDDALACRRLTD-----	GN---	FKVGVHIADVSYFVPEGSSLDKV			
CE-Q09568-LOBO	299	EY-----	RRDFRSDIVFTIDPKTARDLDDALHAKHIDDCGKGTGPGLEIGVHIADVTHFVKPNTSMDSE	GT---	FEVGVHIADVTHFVKPNTSMDSE			
SP-Z99259	438	KK-----	RRDLRNLITITDPETARDLDDAVSCRALDN-----	GT---	YEVGVHIADVTHFVKPNTSMDSE			
SC-P24276-SSD1	686	EYRN---	FTDTNEYNIFAISELG-WVEFALHVRNNGN-----	GT---	LELGCHVVDVTHSHIEGSSVDRR			
SC-P39112	513	KKSGTDDDRYDFGLRVCIDSETAHEIDGVSVKYGR-----	DGL---	YTLYTHIADPTSMFPESTNVDLF				
		701	711	721	731	741	751	761

Fig. 2f



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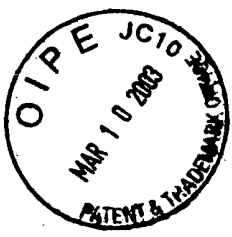
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HS-HMC-Dis3	522	-----SARRGTTVYLCEKRIDMVPELLSS--NLCSLKCDVDRDLAFSCIWEMNHNA-----EILK
MM-hmc-Dis3	522	-----SARRGTTVYLCEKRIDMVPELLSS--NLCSLSNVDRDLAFSCIWEMNHNA-----EILK
CE-Q17632-Dis3	534	-----AALRGTTVYLCDDRIDMLPCLLSS--NLCSLRGEEERYAFSCIWTMTSSA-----DIQS
SP-P37202-Dis3	551	-----AASRGTTVYLVDKRIDMLPMLLGT--DLCSLRPYVERFAFSCIWEMDENA-----NLIK
SC-Q08162-Dis3	586	-----GAARGTSVYLVQKRVVPMPLRLLCE--ELCSLNPMWTDKLTFSVIWKLTPPEG-----KILE
MM-LOBO	424	-----AAERATSVYLVQKRVVPMPLRLLCE--ELCSLNPMWTDKLTFSVIWKLTPPEG-----KILE
HS-LOBO	51	-----AAERATSVYLVQKRVVPMPLRLLCE--ELCSLNPMWTDKLTFSVIWKLTPPEG-----KILD

Fig. 2g





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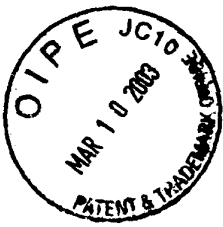
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CE-Q09568-LOBO	363	----	ASERGNSTYLSQTVIPMLPRILCE--	QLCSLNP	GVDRLSFSTVF	KMSYEA	----	ELYD
SP-Z99259	496	----	AASRATTVYLVOKAIPMLPPLICE--	RLCSLNP	NVERLAFSVF	WKLDNGK	----	EICK
SC-P24276-SSD1	746	----	ARKRSSAVFMPQKLVNLLPQSFN--	DELSLAP	GKESATLSVV	YTLDSSTL	----	RIKS
SC-P39112	578	----	GISTDILNVALKRSFTTYLPDTVV	PMLPQS	ICHLSDLGKQ	QORTKTSF	SV	DKITSKCSGKSIEIMYDS
		771	781	791	801	811	821	831
HS-HMC-Dis3	574	TKFTKSVINSKASL-YAEAQLRIDSANMND	----	----	----	----	----	----
MM-hmc-Dis3	574	TRFTKSVINSKASL-YAEAQMRIDSAMND	----	----	----	----	----	----
CE-Q17632-Dis3	586	VKYHKSLIKSKAALTYEKAQEI	IDDPKEQN	----	----	----	----	----
SP-P37202-Dis3	603	VHFTKSVIASKEAFSYADAQAR	IDDKMQD	----	----	----	----	----
SC-Q08162-Dis3	638	VNFMKSVIRSREAFSYEAQALR	IDDKTQND	----	----	----	----	----
MM-LOBO	476	EWFGRTIIRSCTKLSYDHAQSMIEN	PTTEKIP	EEELPPI	SPEHSVEEVHQA	VNLHSGIA	QALRQR	FVDGA
HS-LOBO	103	EWFGRTIIRSCTKLSYDHAQSMIEN	PTTEKIP	EEELPPI	SPEHSVEEVHQA	VNLHSGIA	QALRQR	FVDGA
CE-Q09568-LOBO	415	VWFGRSVIRSRVKLAYEHAQDF	IENPEK	DFTCDEL	PDISDGN	TPFEIKEK	TLMLHRIA	QVLRQKREDSGA
SP-Z99259	549	RWFGKTVIKTCARLAYSEAQGV	IEGKSWDD	AVG--	KPIGG	THTPK	DDVETS	SILTLC
SC-P24276-SSD1	798	TWVGESTISPSNLSLEQLDEKL	STGSPTS	----	----	----	----	----
SC-P39112	648	FKIRKGIVSNFPKATYEDVDR	ILGTPNSEAS	----	----	----	----	----
		841	851	861	871	881	891	901

Fig. 2h



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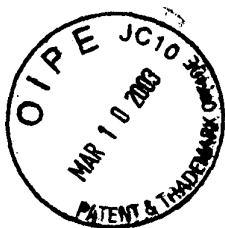
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HS-HMC-Dis3	628	LTLSSPEVRFHMDSETHDPIDLQTKELRETNSMVVEEFMLLANISVAKKIHEEFSEHALLRKHPPAPPPS
MM-hmc-Dis3	628	LTLSSPEIRFHMDSETHDPIDLQTKELRETNSMVVEEFMLLANISVAKKIHEEFSEHALLRKHPPAPPPS
CE-Q17632-Dis3	641	LTLASSEVRFHMDSETHDPIDLQTKELRETNSMVVEEFMLLANISVAKKIHEEFSEHALLRKHPPAPPPS
SP-P37202-Dis3	658	LNLASPEVRIQTDNETSDPMDVEIKQLLETNSLVEEFMLLANISVAKKIHEEFSEHALLRKHPPAPPPS
SC-Q08162-Dis3	693	LNLASPEVKVHMDSETSDPNEVEIKLLATNSLVEEFMLLANISVAKKIHEEFSEHALLRKHPPAPPPS
MM-LOBO	546	LRLDQLKLAFTLDHETGLPQCHIEYRDNSKLVVEEFMLLANISVAKKIHEEFSEHALLRKHPPAPPPS
HS-LOBO	173	LRLDQLKLAFTLDHETGLPQCHIEYRDNSKLVVEEFMLLANISVAKKIHEEFSEHALLRKHPPAPPPS
CE-Q09568-LOBO	485	LRIELPRLKFALDEDK-KPQGVSIYEIKDSNKLVEEFMLLANISVAKKIHEEFSEHALLRKHPPAPPPS
SP-Z99259	617	VEINSTEKLFQDEYG-MPNKCEVYEQTDANHLIEEFMLLANISVAKKIHEEFSEHALLRKHPPAPPPS
SC-P24276-SSD1	849	ATLPTLSLLESLDEKVKVDNLDRTLGLFWINEIKRKNSTVAEKIYTKLGDALLRRQMPIATKM
SC-P39112	704	AVIFGEGFNKGLVMLN---ADSEGELETEVTFSDQEETLSLIVSEMMILANTLTGRYFAEN---KI
	911	921 931 941 951 961 971
HS-HMC-Dis3	698	EILVKAARS-RNLEIKTDTAKSLAESLDQAESPTFPYLN---TLRLILATRCMMQAVYFCSGMD---
MM-hmc-Dis3	698	DILVKAARS-KNLQIKTDTAKSLADSLDRAESPDFFPYLN---TLRLILATRCMMQAVYFCSGMD---
CE-Q17632-Dis3	711	KPLVEAARH-RGFELIIVESGKGLADSLNRCVDDKKNPMLN---RLRLMLTTRCMTQAVYFSAGKDGFS
SP-P37202-Dis3	728	DSLQDILRVCKGMHLKCDTSKSLAKSLDECVDPKEPYFN---TLRLILATRCMLSAEYFCSGTFAP---
SC-Q08162-Dis3	763	EILNEMLNTRKNMSISLESSKALADSLDRCVDPEDPYFN---TLVRIMSTRCMMQAVYFSAGYSY---
MM-LOBO	616	SDLVEFCDO-MGLPMDVSSAGALNKSLTKTFGDDKYSLARKEVLTNNMYSRPMQMALYFCSGMLQD---
HS-LOBO	243	SDLVEFCDO-MGLPMDVSSAGALNKSLTKTFGDDKYSLARKEVLTNNMYSRPMQMALYFCSGMLQD---
CE-Q09568-LOBO	554	KDVAEQCAR-IGFPLDGRTSGLLSLTKYQKSRIDMCIRQVSSLTIKPMQQAQYFCT--FEM---
SP-Z99259	686	NEFCHFLKS-MNFDFFDASSAFAFNASMVRLRSTFNEELV---ELFENMAVRSLNRAEYFCTGDFGEK---
SC-P24276-SSD1	919	ASFRKKIQN-FGVNFDNTADELIKGVKIKDDDDVRVGI---EILLFKTMRPRARYFIAGKVD---
SC-P39112	764	GGVFCYKQ---LPLGEVAQQQYDSMITSTKKGIFPKLK---DIVKLSLLNSSFYTGPRFR---
	981	991 1001 1011 1021 1031 1041

Fig. 2i



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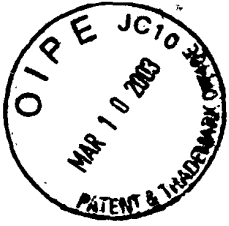
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HS-HMC-Dis3	758	-----	ND	-----	FHHYG	-----	FHHYG
MM-hmc-Dis3	758	-----	ND	-----	FHHYG	-----	FHHYG
CE-Q17632-Dis3	778	EEKKFFVLKTLNLPYRSCLCDDTETSIHLSRGLNDYFLFKKEKLHMSVGLFKLFDCLGTVPVPQYQHFG	-----	-----	-----	-----	-----
SP-P37202-Dis3	791	-----	PD	-----	FRHYG	-----	FRHYG
SC-Q08162-Dis3	826	-----	PD	-----	FRHYG	-----	FRHYG
MM-LOBO	680	-----	QEQR	-----	HYA	-----	HYA
HS-LOBO	307	-----	PAQFR	-----	HYA	-----	HYA
CE-Q09568-LOBO	616	-----	PLSFYH	-----	HFA	-----	HFA
SP-Z99259	749	-----	TD	-----	WHHYA	-----	WHHYA
SC-P24276-SSD1	977	-----	PDQ	-----	YGHYA	-----	YGHYA
SC-P39112	820	-----	-----	-----	HEM	-----	HEM
	1051	-----	1061	1071	1081	1091	1101
		1111					
HS-HMC-Dis3	765	LASPIYTHFTSPIRRYADVIVHRLLAIVAIGADCTYPELTDFHKLADICKNLNFRHKMAQYASVAFHT	-----	-----	-----	-----	-----
MM-hmc-Dis3	765	LASPIYTHFTSPIRRYADVIVHRLLAIVAIGADCTYPELTDFHKLADICKNLNFRHKMAQYASVAFHT	-----	-----	-----	-----	-----
CE-Q17632-Dis3	848	LACAIYTHFTSPIRRYADVIVHRLLAIVAIGADCTYPELTDFHKLADICKNLNFRHKMAQYASVAFHT	-----	-----	-----	-----	-----
SP-P37202-Dis3	798	LASPIYTHFTSPIRRYADVIVHRLLAIVAIGADCTYPELTDFHKLADICKNLNFRHKMAQYASVAFHT	-----	-----	-----	-----	-----
SC-Q08162-Dis3	833	LAVDIYTHFTSPIRRYADVIVHRLLAIVAIGADCTYPELTDFHKLADICKNLNFRHKMAQYASVAFHT	-----	-----	-----	-----	-----
MM-LOBO	688	LNVPLYTHFTSPIRRYADVIVHRLLAIVAIGADCTYPELTDFHKLADICKNLNFRHKMAQYASVAFHT	-----	-----	-----	-----	-----
HS-LOBO	315	LNVPLYTHFTSPIRRYADVIVHRLLAIVAIGADCTYPELTDFHKLADICKNLNFRHKMAQYASVAFHT	-----	-----	-----	-----	-----
CE-Q09568-LOBO	625	LNVPLYTHFTSPIRRYADVIVHRLLAIVAIGADCTYPELTDFHKLADICKNLNFRHKMAQYASVAFHT	-----	-----	-----	-----	-----
SP-Z99259	756	LNVPLYTHFTSPIRRYADVIVHRLLAIVAIGADCTYPELTDFHKLADICKNLNFRHKMAQYASVAFHT	-----	-----	-----	-----	-----
SC-P24276-SSD1	985	LNVPLYTHFTSPIRRYADVIVHRLLAIVAIGADCTYPELTDFHKLADICKNLNFRHKMAQYASVAFHT	-----	-----	-----	-----	-----
SC-P39112	823	IGAKQYLTVTSPLRRFPDLINHLQIHRHLQ-----	-----	-----	-----	-----	-----
	1121	-----	1131	1141	1151	1161	1171
		1181					

Fig. 2j



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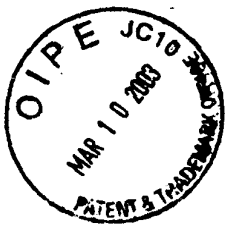
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HS-HMC-Dis3	835	QLFFKSKG-----IVSEEAYILFVRKNAIVVLIIPKYGLEGTVFFFEKDKPNPQLI-----
MM-hmc-Dis3	835	QLFFKSKG-----IVSEEAYILFVRKNAIVVLIIPKYGLEGTVFFFEKDKPKPRLA-----
CE-Q17632-Dis3	918	VRYFKGK-----VETCEGFVMGVRNNGIQVFPKYGLESIIVLQTSAAAG--TT-----
SP-P37202-Dis3	868	GQALKGG-----VAEEDAYVIVKVFKNNGFVFIARFGLGEGIVYTKSLSSVLEPN-----
SC-Q08162-Dis3	903	GQVMRNN-----ESTETGYVIVKVFNNNGIVLVLPKFGVEGLIRLDNLT--EDPNS-----
MM-LOBO	756	AVLVKESG-----PLESEAMVMGVLNQAFDVLVLRFGVQKRIYCNALALRSYSFQ-----
HS-LOBO	383	AVLVKESG-----PLESEAMVMGILKQAFDVLVLRFGVQKRIYCNALALRSYHFQ-----
CE-Q09568-LOBO	693	GVFIHQTG-----PMKCQAVVLGVMDLSFDVLIVEYGVVKKRVYVDKMKR---DFN-----

Fig. 2k



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SP-Z99259	823	SVYIAEYCKKHKKMPVQAFATRISGNSIDVYISEYGISNRVDLSSDDR-IKSF	1191	1201	1211	1221	1231	1241	1251
SC-P24276-SSD1	1052	CKTINDMGNTTG--QLLTMTATVLQVYESSFDVFIPEFGIEKRVHGDQLPLIKAEDGTNRVLELHWQPGV							
SC-P39112	890	LNYLKKL-----TKLEPERTFDVMVT-----SVPQNGFTGCVFPDLSFARGTLK-----							
			1191	1201	1211	1221	1231	1241	1251
HS-HMC-Dis3	885	-----YDDEIPSLKIED-TVFHVFDKVKVKIMLDSSNLOHQKIRMSLIVEPQIPGIS							
MM-hmc-Dis3	885	-----YDDEIPSLRIEG-TVFHVFDKVKVKITLDSSNLOHQKIRMAIVEPQIPGIN							
CE-Q17632-Dis3	965	-----IDVEEMSVKVGNDWVWIKELPVTVRISVNEKNQQRPRVELQLIKPAIPGLS							
SP-P37202-Dis3	916	-----VEYVEDEYKINI--EIRDQPKPQT---VQIQMFQQVVRVTVTVRDEHSGKQ							
SC-Q08162-Dis3	950	-----AAFDEVEYKLTFF--VPTNSDKPR-----DVYVFDKVEVQVRVSVMDPITSKR							
MM-LOBO	806	-----KVGKKPELTLVWEPD-DLE---EEPTQQVITIFSLVDVVLQAEATALKYSA							
HS-LOBO	433	-----KVGKKPELTLVWEPE-DME---QEPAQQVITIFSLVEVVLQAEATALKYSA							
CE-Q09568-LOBO	740	-----KSTK--LTIYWPADPNABSGNREEFSSSIQMCNVVYVIL-VPYKSIEVSA							
SP-Z99259	878	-----VAPDDSSVKITL---FDDS---Q-K---TIALTDRFQVYLYSDYSRTFFSI							
SC-P24276-SSD1	1120	DSATFPADEKNPKSYRNSIKNFRSTAAEIANIELDKAESEPLISDPLSKELSDHLTVPNLRLPSAS							
SC-P39112	934	-----LHPSSMHYPMIG-----DIVKNCKISKIDCLEGMLELEKL-----							
			1261	1271	1281	1291	1301	1311	1321

Fig. 21



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HS-HMC-Dis3	935	IPTDTS	NMDLNGPKKKMKLGK	1331
MM-hmc-Dis3	935	IPPVNA	DKALTPAGGKKRKLEK	1341
CE-Q17632-Dis3	1016	V	DFDLSSEG	1351
SP-P37202-Dis3	962	K	QITLVY	1361
SC-Q08162-Dis3	994	K	ELLK	1371
MM-LOBO	853	ILKRP	LEKASDEEPED	1381
HS-LOBO	480	ILKRPQTQHLGPEKEEESDGEPEDSSTS		
CE-Q09568-LOBO	788	TIVRPS	LEQRNILKSTLKDMMKETGSTILO	
SP-Z99259	919	R	CSLVSLN	
SC-P24276-SSD1	1190	DNKQNALEKFISTETRIENDNYIQEIHELQKIPILLRAEVMALPCLTVRALNPFMKRV		

Fig. 2m

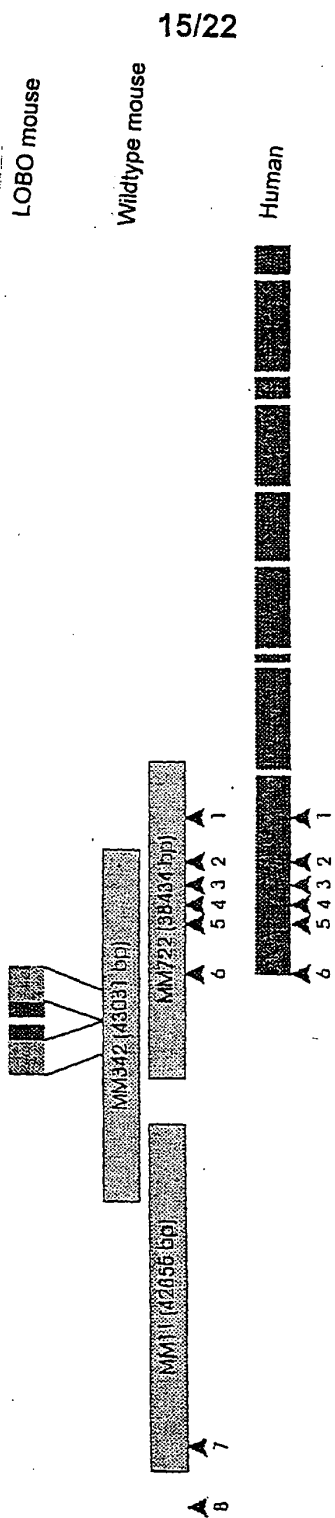


Fig. 3

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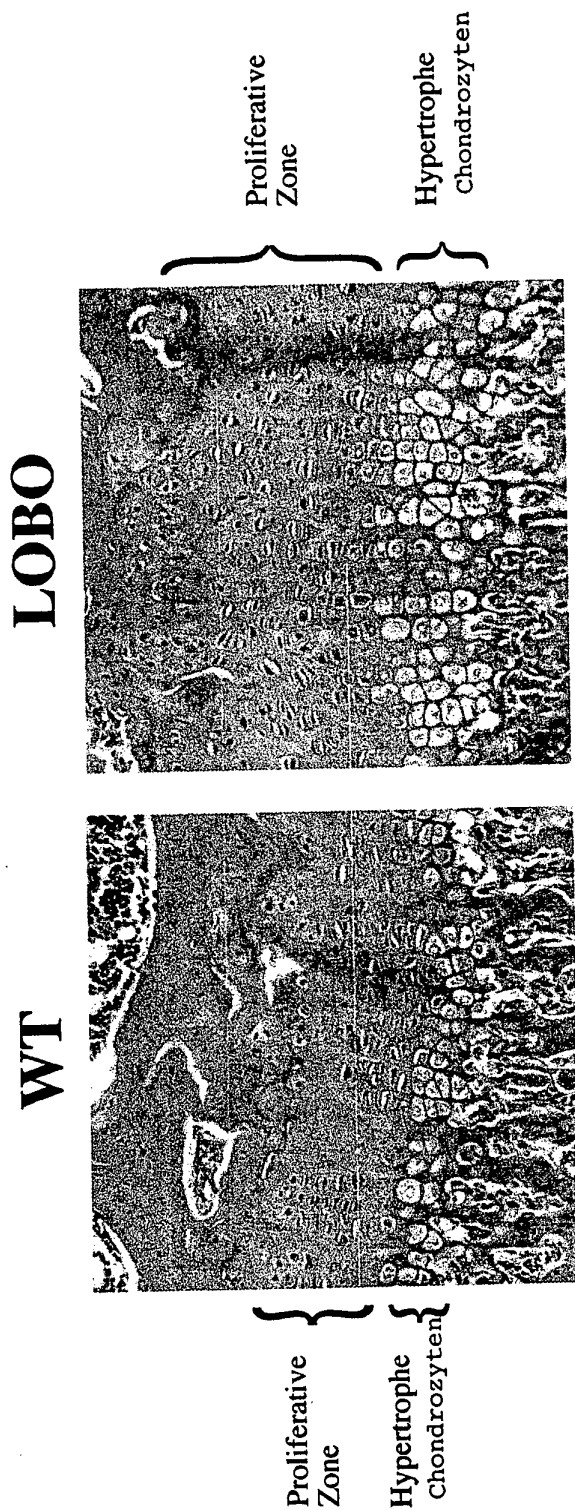
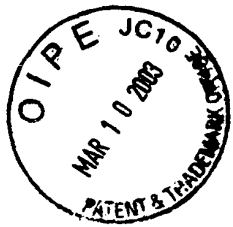


Fig. 4





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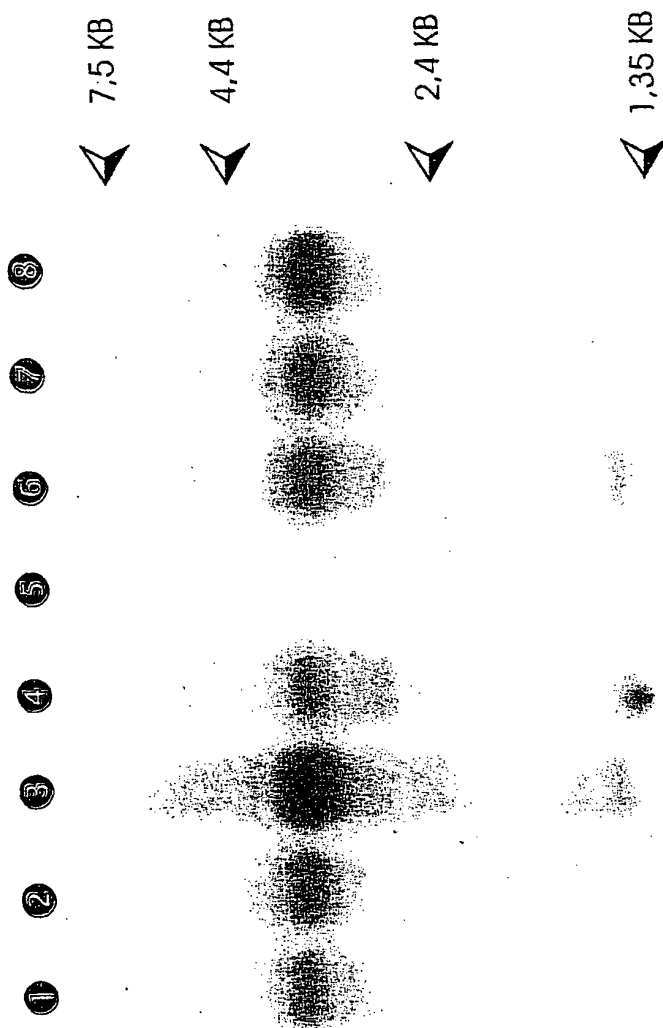
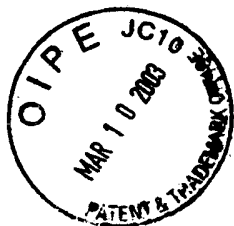


Fig. 5



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## Dis3 Proteins

## VACB / RNase II

## LOBO

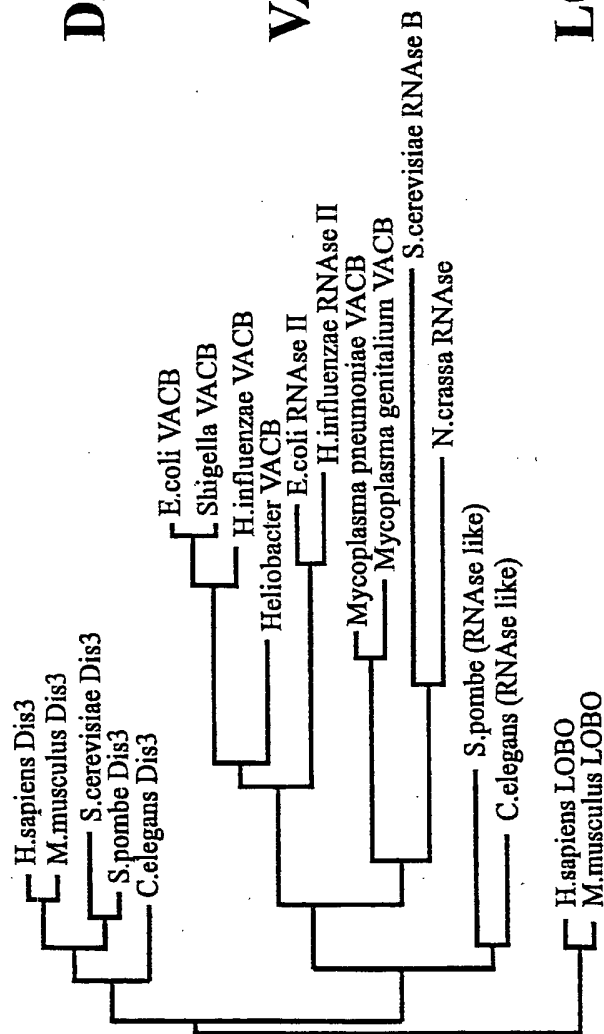


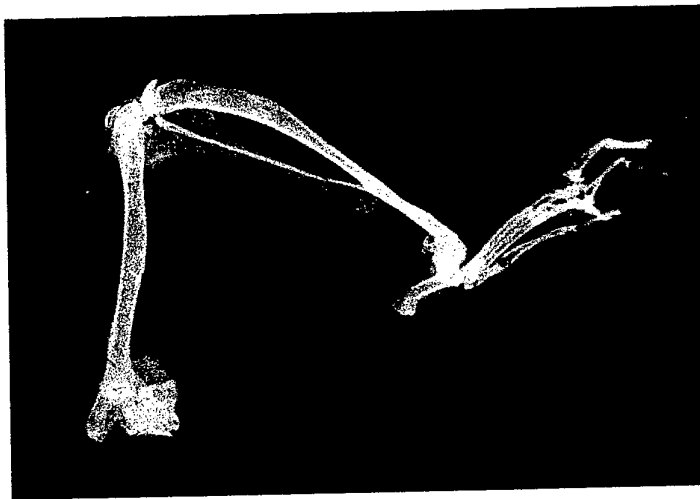
Fig. 6

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LOBO



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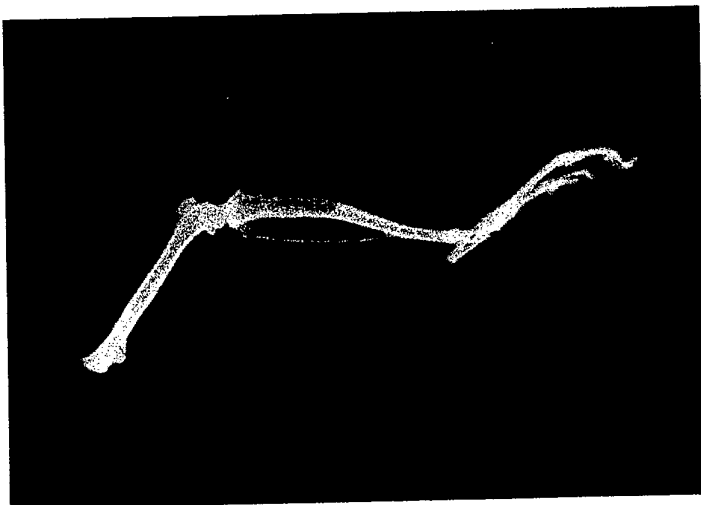
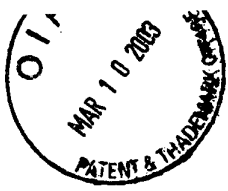


Fig. 7



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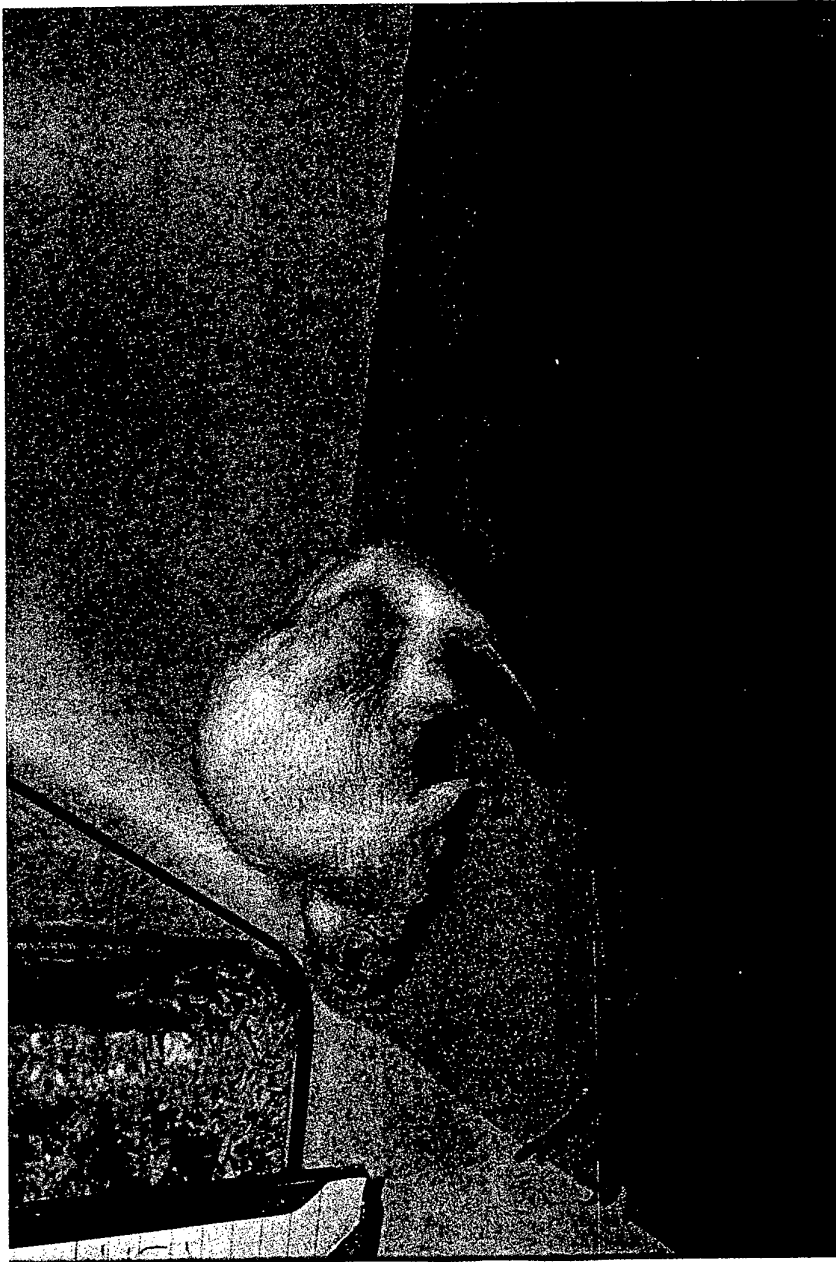


Fig. 8

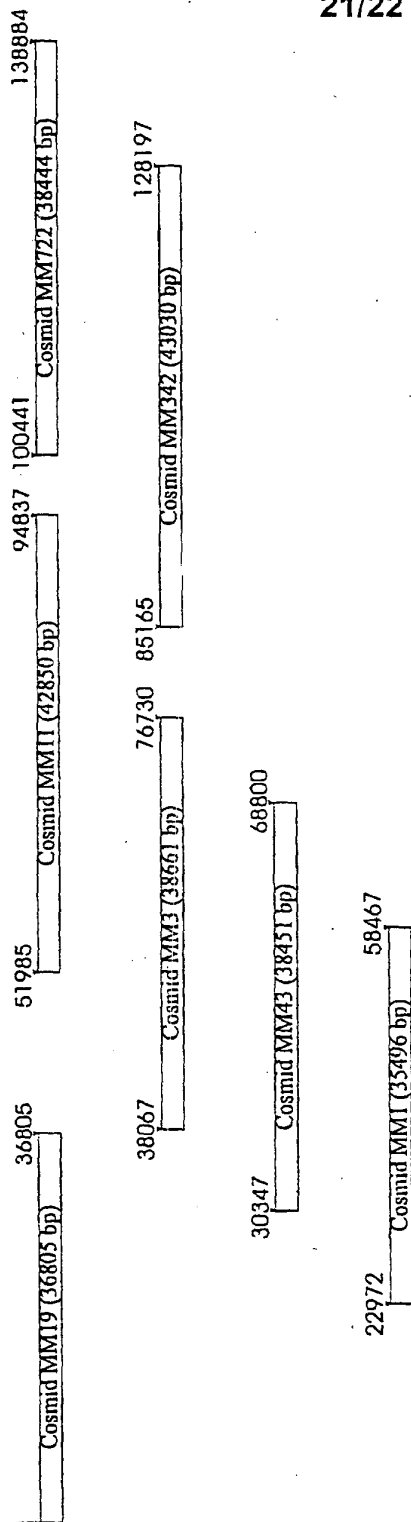


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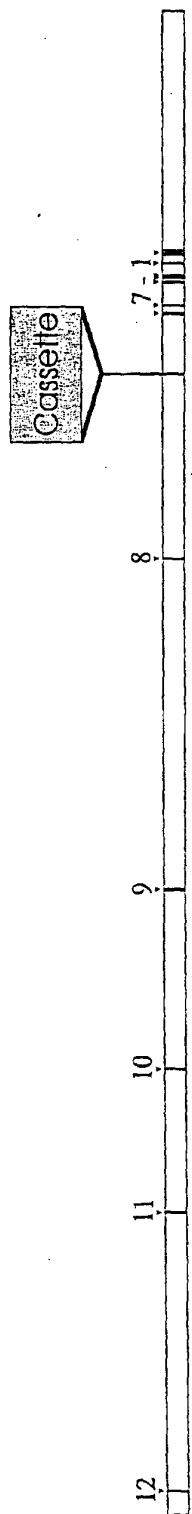
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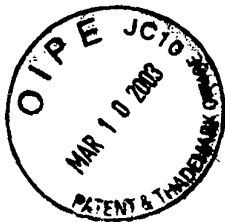


A

Fig. 9



B



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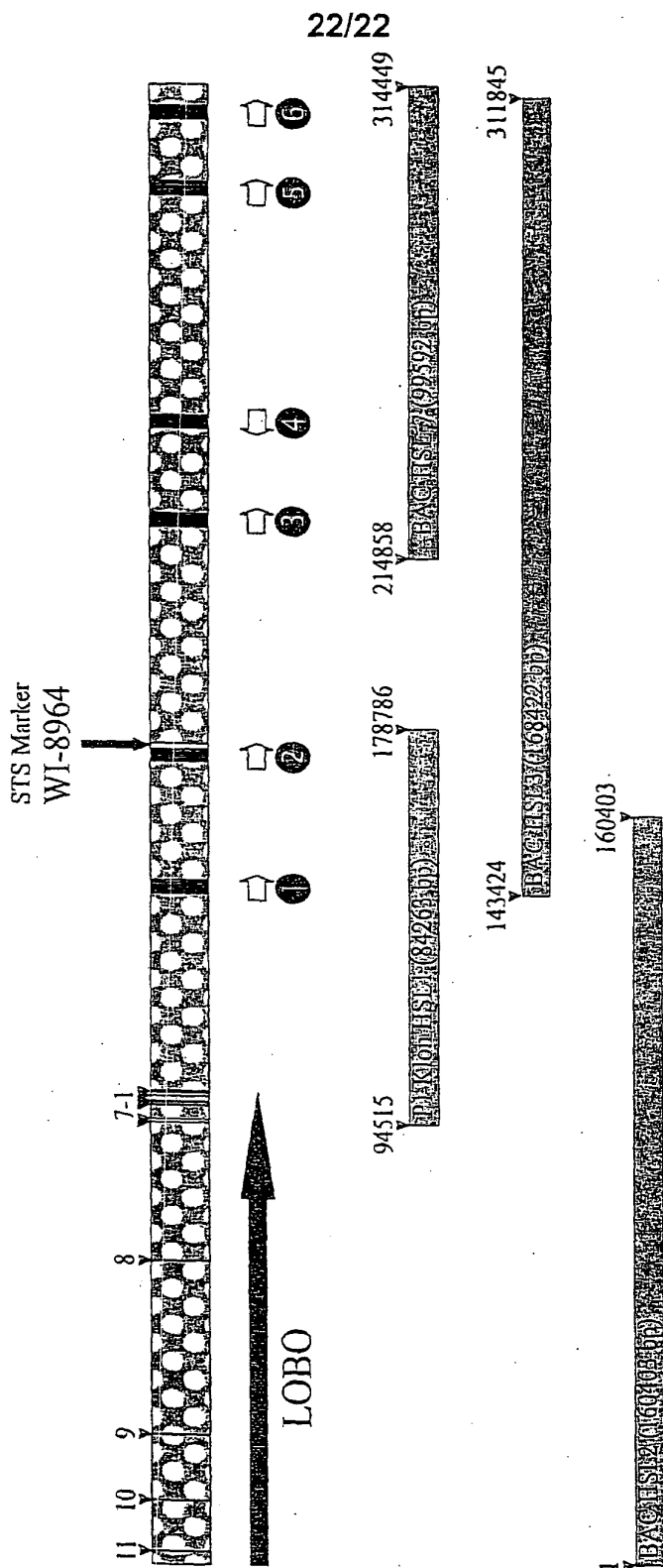


Fig. 10